CONVERSION OF CODONS INTO ANALOGOUS CONFORMERS, AND ASSEMBLY OF CONFORMERS INTO POLYPEPTIDES

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This article is a supplement to "Evidence for the Existence of an Intelligible Genetic Code," in the previous issue of the Quarterly, as was proposed in that article. More information on the constructions mentioned in the first article are provided for those who may want to assemble the models described.

Procedure for Conversion of Codons into Analogous Conformers

In genetic translation of mRNA into corresponding polypeptides, the recognized high fidelity of the process depends on accurate recognition of mRNA codons by homologous tRNA anticodons. Recognition, in chemical terms, consists of the close fitting together of A:U and G:C homologous base pairs when the nucleotides to which they belong are in fully extended or "anti" conformation.

Not only are homologous base pairs complementary in shape at points of contingence, but they also produce strong hydrogen bonds at these apposed points, namely: N-3 and O-4 of uridine (U) bond to N-1 and N-6 of adenine (A), respectively; O-2, N-3, and N-4 of cytosine (C) hydrogen-bond to N-2, N-1, and O-6 of guanine (G), respectively. These base-pairing patterns are illustrated in Figure 1.

Usually, a codon such as GGG for Gly is recognized preferentially by the expected homologous anticodon of tRNA, namely CCC. However, on occasion, when three bases such as G,G,U are assembled into a trinucleotide such as GGU for Gly, electrical charges on the potential H-bonding sites of component bases are so altered that the expected hydrogen-bonding patterns with the predicted anticodon, in this case ACC, cannot develop.

It has been shown that the genetic machinery anticipates this problem by first forming the expected anticodon ACC, and then directing the enzyme adenosine deaminase to convert the N-6 amino group of adenosine to an O-6 group, thereby forming inosine (I). The resulting modified anticodon ICC very effectively recognizes Gly codon GGU in the translation process.

The characteristic shape of each subspecies of isoaccepting tRNA molecule is determined by the specific patterns of base-pairings which form among the 80 or more component bases in a tRNA molecule; also, the spatial orientation of an amino acid covalently bound to its unique subspecies of isoaccepting tRNA is controlled by the pattern of hydrogen bonds formed between juxtaposed O and N groups of the amino acid and certain bases of the tRNA. This multiple-bond linkage insures that the bound amino acid will be held in a specific 3-D conformation as it is presented to the ribosome by tRNA during the translation process.

This 3-D conformation for the amino acid, the conformer, permits the establishment of the proper hydrogen bonds, hydrophobic interactions, and disulfide bridging with the existing polypeptide at the moment of peptide bond formation. The loaded tRNA needs to hold its conformer burden on the ribosome

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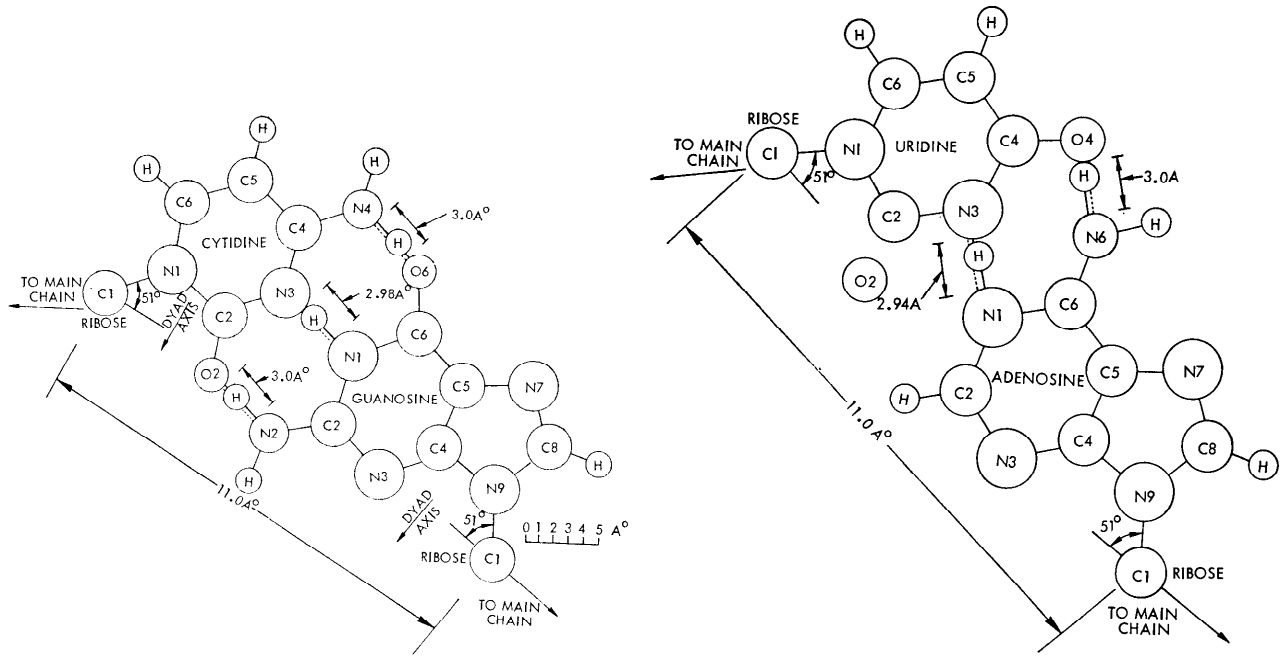

Figure 1. Watson-Crick hydrogen bond pairing of RNA bases between guanosine and cytidine (left) and between adenosine and uridine (right).

for only 1/50th second before peptide bonding is completed enzymatically, and the covalent linkage of amino acid to tRNA is broken simultaneously, also enzymatically.

In this direct control of polypeptide shape by specific mRNA codon sequences, each conformer is functioning as an analog of the corresponding codon.

The assignment of a conformer to each of the 64 mRNA codons was conducted in a somewhat arbitrary, but consistent, fashion as follows:

Step 1. As illustrated in Table 1, codons may be converted logically into analogous binary arithmetic numbers, or binary codons; in this system, the binary codon is the binary arithmetic complement of the binary anticodon, and vice versa.

Step 2. Since the hydrogen-bonding potentialities of codon and anticodon trinucleotides are determined by the relative distributions of electropositive and electronegative charges at contingent sites, a dynamic representation of the binary codon is an obvious requirement for conversion of mRNA codons into conformer analogs. In other words, a method must be employed for conversion of the static "1" bits into functional representations of positive charges, and for conversion of "0" bits into functional representations of negative charges.

Since the electrostatic charges involved in H-bonding behave somewhat like small magnetic fields, it seemed feasible to represent "1" bits as N polarity, and "0" bits as S polarity of bar magnets. This conversion of binary codon to its equivalent magnetic codon is illustrated in Figure 2 which shows the spontaneous deflections of the array of magnets produced by interacting polarities.

Step 3. Since the conformer is considered to be the analog of the corresponding mRNA codon, it is logical to relate the angular deflections representing a given magnetic codon to a set of angular rotations of the corresponding amino acid that will give rise to the spatial orientation of the conformer. This conversion of rotational angles to representations of the

Table 1. Steps in conversion of codons into conformers. This same table was given in the article, "Evidence for the Existence of an Intelligible Genetic Code"; and is reproduced here for convenience.

Amino Acid Conformer	Trinucleotide Codon Acronym	Binary Codon	Magnetic Codon	Rotational Angles for Amino and Carboxyl Groups in x, y, z planes					
Gly-1	GGG	000000	SSSSSS	0	0	0	0	0	0
Gly-2	GGA	000001	SSSSSN	300	300	300	300	300	60
Gly-3	GGU	000010	SSSSNS	0	0	0	0	270	0
Gly-4	GGC	000011	SSSSNN	340	340	340	340	70	70

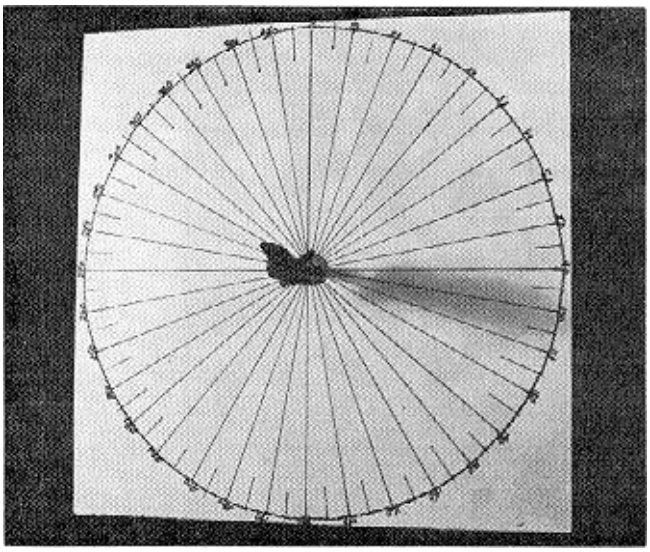

Figure 2. Device to convert binary codons to magnetic codons. A protractor is drawn on a board. At the center is an axle, on which magnets are placed so as not to prevent rotation. In the case shown here, it will be noticed that some are at 60 degrees, some at 300 degrees.

It might be remarked that the magnets, due to interaction, will move into a configuration in which their energy is a minimum, subject to the constraints. A similar principle applies to the interaction of electric charges, as is mentioned in the text. Thus the arrangement of magnets might be considered a sort of analogue computer, to investigate the interaction of the electric charges which, in turn, determine the interaction of the molecules concerned.

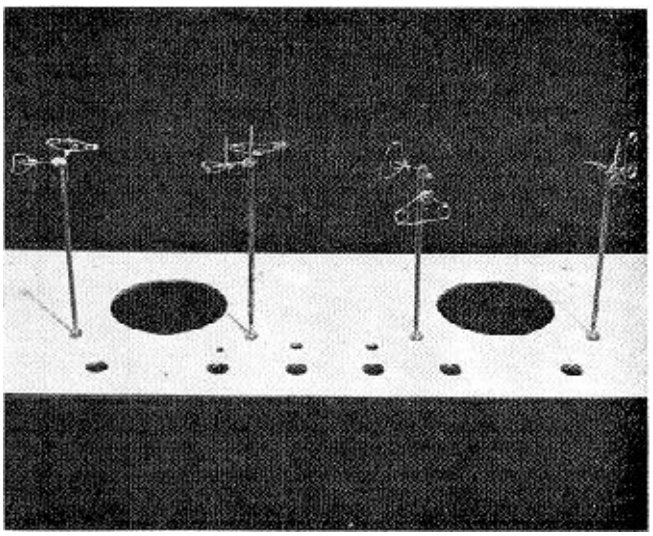

Figure 3. The four conformers of Glycine, as Kendrew Wire Scale Models, shown here in a top view. This is Figure 1 (b) of the article, "Evidence for the Existence of an Intelligible Genetic Code," reproduced here for convenience.

conformers of amino acids was carried out in the following manner:

A Kendrew wire model of the amino acid backbone (shown in Figure 3) was mounted on the stage of a Leitz-Wetzlar universal stage with the amino-terminus to the left on the east-west axis, as viewed from the normal position of a microscope operator. This amino acid conformation corresponds to the orientation of Gly-1 conformer that is shown in Figure 4.

All rotational angles were read clockwise, as viewed from above the "top-side" of the amino acid backbone. In a few cases, where the rotational angles were close to 180°, it was convenient to invert the entire instrument to facilitate setting the angles.

Reading from left to right, the six angles generated by magnetic codons were applied to the amino acid model as follows:

(a) Rotation of the amino group around the C^{α}, in the horizontal plane.
(b) Rotation of the amino group around the N-C^{α} axis in a plane that is perpendicular both to the horizontal plane and to the N-C^{α} axis.
(c) Rotation of the amino group about the C^{α} in a plane that is perpendicular to the other two planes.
(d) Rotation of the carboxyl group around the C^{α} in the horizontal plane.
(e) Rotation of the carboxyl group around the C′-C^{α} axis in a plane that is perpendicular both to the horizontal plane and to the C′-C^{α} axis.
(f) Rotation of the carboxyl group around the C^{α} in a plane that is perpendicular to the other two planes.

It will be noted that conformer Gly-1, which is the analog of the first mRNA codon for Gly, has the orientation of the reference amino acid backbone model since all angles produced by the corresponding magnetic codon, SSSSSS, are zero in magnitude. The remaining three mRNA codon synonyms for Gly, however, transform into Gly conformers with characteristic spatial orientations, as represented in Figure 4.

To facilitate orientation of scale models of amino acids into conformers, the Cartesian coordinates on X, Y, and Z axes were determined for each atomic center in each different conformer, using a scale of 1 cm per Å. As an illustration, the 3-D coordinates for the four Gly conformers are listed in Table 2.

Procedure for Assembly of Conformers into Polypeptides

Protein chemists have established a standard conformation of an amino acid as the reference position from which all angular rotations of the amino acids in a polypeptide may be measured. This standard conformation of an amino acid is that of Gly-1 conformer, as shown in Figure 4.

A second convention of protein chemistry is that in polypeptide synthesis, peptide bonds are formed to the right during genetic translation of mRNA; the C-2 group to the left links with the N-1 group of the next amino acid to be joined to the growing peptide chain.

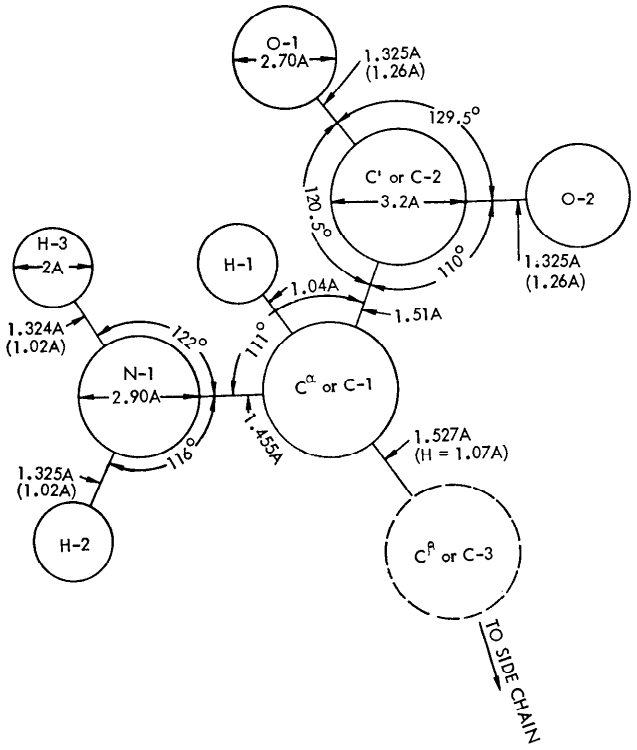

Figure 4. Amino acid backbone structure in standard reference configuration.

As mRNA translation starts, considerable freedom of choice exists for spatial orientation of amino acid residues forming the first peptide bond, for aside from avoiding steric hindrance, these amino acid residues need only abide by the restriction that their C-1 or C^{α} groups must lie about 3.8 Å apart. An additional restraint is introduced, however, as the second peptide bond links the third amino acid residue to the polypeptide, for now the second peptide bond must be formed in "trans" or staggered configuration with respect to the initial peptide bond.

To illustrate, if the first peptide bond involved O-1 of the first amino acid residue and H-2 of the second amino acid, the third amino acid must bond to O-2 of the second amino acid rather than to O-1; this trans pattern is continued on down the polypeptide chain of normal proteins.

As the polypeptide chain lengthens, the bulky sidechains of amino acid residues introduce additional restraints on the allowable conformations. When conformers are fitted together in peptide linkages, they must be able to anticipate not only how they should bond to their nearest neighbors, but also how they must position their sidechains to leave space for conformers yet to be added at much more distant regions of the chain.

When a specific mRNA codon sequence is translated into assembled conformers, as illustrated in Figures 2-5 of the article "Evidence for the Existence of an Intelligible Genetic Code," the individual conformers are held in their typical 3-D orientation until the peptide bond has been formed.

Table 2. Coordinates for glycine conformers.

GGG = 000000 = Gly-1

Atoms	X-axis	Y-axis	Z-axis
C.1	30.5	30.5	30.5
C.2	32.1	30.5	30.5
C.3	33.1	26.7	30.5
H.1	28.3	33.5	30.5
H.2	23.1	28.7	30.5
H.3	24.0	33.5	30.5
N.1	26.0	30.5	30.5
O.1	29.4	37.0	30.5
O.2	36.2	35.9	30.5

GGA = 000001 = Gly-2

Atoms	X-axis	Y-axis	Z-axis
C.1	30.5	30.5	30.5
C.2	31.7	31.2	33.5
C.3	31.5	32.2	25.0
H.1	26.3	27.8	32.0
H.2	24.0	30.8	27.3
H.3	23.3	27.7	32.7
N.1	24.7	29.4	30.5
O.1	29.0	27.8	36.0
O.2	35.9	29.0	33.2

GGU = 000010 = Gly-3

Atoms	X-axis	Y-axis	Z-axis
C.1	30.5	30.5	30.5
C.2	31.5	30.5	25.3
C.3	31.6	30.5	34.0
H.1	28.8	30.5	27.5
H.2	23.8	30.5	33.1
H.3	23.3	30.5	27.7
N.1	25.5	30.5	29.8
O.1	28.5	30.5	22.4
O.2	36.0	30.5	25.5

C radius = 1.6A
H radius = 1.0A
O, N radii = 1.3A
C^{α} = C.1

GGC = 000011 = Gly-4

Atoms	X-axis	Y-axis	Z-axis
C.1	30.5	30.5	30.5
C.2	33.1	36.0	30.5
C.3	29.0	28.3	26.4
H.1	30.8	32.7	32.5
H.2	27.3	26.0	34.5
H.3	31.3	31.2	37.1
N.1	30.5	29.5	34.0
O.1	32.7	36.5	33.2
O.2	33.5	36.2	26.0

C′ = C.2
C^{β} = C.3

After assembly, the conformers must remain in their initial conformations to enable the normal hydrogen bonding patterns to occur. These hydrogen bonds are simulated by soldering connecting wires of 3.0 Å length between the H-bonded sites.

After the entire polypeptide chain has been produced, disulfide bonds can be inserted between the appropriate half-cysteine residues; the formation of these disulfide bridges usually requires that segments of the polypeptide chain must move with respect to the recognized "hinge" regions to permit the 3.75 Å disulfide bridge to form.

NEW CREATIONISTIC PUBLICATION

The journal *Origins* is now being published by the Geoscience Research Institute, Loma Linda University, Loma Linda, California 92354. The present intention is to publish it twice a year. Two issues appeared in 1974 and Volume 2, Number 1 was received recently.

The topics treated are of the same general nature as those in the C.R.S. *Quarterly*. Issues mentioned, for instance, have contained very good discussions of fossil trees, creation-flood model, "growth lines" in invertebrates, and C-14 age profiles for ancient sediments.

Appearance of another publication devoted to these matters is good news. The field which might be called, "Creation Science," is wide enough for many teams. And if creationists in various scientific disciplines work faithfully, there will be results enough to fill several journals.

ANOTHER CREATIONISM PUBLICATION

The editor recently saw the publication, *Folha Criacionista*, published by the Sociedade Criacionista Brasileira, Caixa Postal, 274, 13560 Sao Carlos—S.P., Brazil. The particular issue was Volume 3, Number 6, April, 1974. It contained work by such well known authors to the Creation Research Society as William J. Tinkle and Edgar C. Powell.

An editorial mentions the distribution of literature, not only in Brazil, but also in other parts of South America. It is good to see the work of creationism being taken up in so many parts of the world.

—Contributed by Harold Armstrong